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**BOX PCT**

In re International Patent Application of

**DUKE UNIVERSITY ET AL**

Agent's File Ref: 1579-379

International Application No: **PCT/US99/17678**  
International Filing Date: 05 August 1999

For: URATE OXIDASE

19 November 1999

United States Receiving Office  
Honorable Commissioner of Patents  
and Trademarks  
Washington, D.C. 20231

**Response to Correct Defects in International Application**

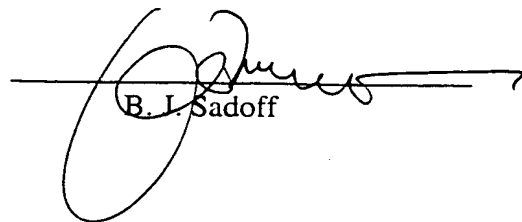
Dear Sirs,

Attached is a printed sequence listing for this application and a copy of the computer readable form on a 3.5" disk in the attached envelope.

In accordance with 37 CFR 1.821-1.825, I hereby state that the content of the paper and computer-readable copies of the sequence listing submitted in accordance with 37 CFR 1.821(c) and (e), respectively, are the same. I hereby state that the submission, filed in accordance with 37 CFR 1.821(g), does not introduce new matter.

Respectfully submitted,

**NIXON & VANDERHYE P.C.**

  
B. I. Sadoff

8th Floor  
1100 North Glebe Road  
Arlington, Virginia 22201-4714

## SEQUENCE LISTING

<110> HERSHFIELD, MICHAEL S.  
KELLY, SUSAN J.

<120> URATE OXIDASE

<130> 1579-379

<140> PCT/US99/17678

<141> 1999-08-05

<160>11

<170> PatentIn Ver. 2.0

<210> 1

<211> 915

<212> DNA

<213> Artificial Sequence

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<221> CDS

<222> (1)..(915)

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<223> Description of Artificial Sequence:PBC CHIMERA

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Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln	
20 25 30	

cga gat gga aaa tat cac agc att aaa gag gtg gca act tca gtg caa	144
Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln	
35 40 45	

ctg act ttg agc tcc aaa aaa gat tac ctg cat gga gac aat tca gat	192
Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp	
50 55 60	

gtc atc cct aca gac acc atc aag aac aca gtt aat gtc ctg gcg aag	240
Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys	
65 70 75 80	

ttc aaa ggc atc aaa agc ata gaa act ttt gct gtg act atc tgt gag	288
Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu	
85 90 95	

cat ttc ctt tct tcc ttc aag cat gtc atc aga gct caa gtc tat gtg	336
His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val	
100 105 110	

gaa gaa gtt cct tgg aag cgt ttt gaa aag aat gga gtt aag cat gtc	384
Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val	
115 120 125	

cat gca ttt att tat act cct act gga acg cac ttc tgt gag gtt gaa	432
His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu	
130 135 140	

cag ata agg aat gga cct cca gtc att cat tct gga atc aaa gac cta 480  
 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu  
 145 150 155 160

aaa gtc ttg aaa aca acc cag tct ggc ttt gaa gga ttc atc aag gac 528  
 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp  
 165 170 175

cag ttc acc acc ctc cct gag gtg aag gac cgg tgc ttt gcc acc caa 576  
 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln  
 180 185 190

gtg tac tgc aaa tgg cgc tac cac cag ggc aga gat gtg gac ttt gag 624  
 Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu  
 195 200 205

gcc acc tgg gac act gtt agg agc att gtc ctg cag aaa ttt gct ggg 672  
 Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly  
 210 215 220

ccc tat gac aaa ggc gag tac tca ccc tct gtg cag aag acc ctc tat 720  
 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr  
 225 230 235 240

gat atc cag gtg ctc tcc ctg agc cga gtt cct gag ata gaa gat atg 768  
 Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met  
 245 250 255

gaa atc agc ctg cca aac att cac tac ttc aat ata gac atg tcc aaa 816  
 Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys  
 260 265 270

atg ggt ctg atc aac aag gaa gag gtc ttg ctg cca tta gac aat cca 864  
 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro  
 275 280 285

tat gga aaa att act ggt aca gtc aag agg aag ttg tct tca aga ctg 912  
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tga 915  
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<210> 2  
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 <212> PRT  
 <213> Artificial Sequence

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 20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln  
 35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp  
 50 55 60

Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys  
 65 70 75 80

Phe	Lys	Gly	Ile	Lys	Ser	Ile	Glu	Thr	Phe	Ala	Val	Thr	Ile	Cys	Glu	85	90	95
His	Phe	Leu	Ser	Ser	Phe	Lys	His	Val	Ile	Arg	Ala	Gln	Val	Tyr	Val	100	105	110
Glu	Glu	Val	Pro	Trp	Lys	Arg	Phe	Glu	Lys	Asn	Gly	Val	Lys	His	Val	115	120	125
His	Ala	Phe	Ile	Tyr	Thr	Pro	Thr	Gly	Thr	His	Phe	Cys	Glu	Val	Glu	130	135	140
Gln	Ile	Arg	Asn	Gly	Pro	Pro	Val	Ile	His	Ser	Gly	Ile	Lys	Asp	Leu	145	150	155
Lys	Val	Leu	Lys	Thr	Thr	Gln	Ser	Gly	Phe	Glu	Gly	Phe	Ile	Lys	Asp	165	170	175
Gln	Phe	Thr	Thr	Leu	Pro	Glu	Val	Lys	Asp	Arg	Cys	Phe	Ala	Thr	Gln	180	185	190
Val	Tyr	Cys	Lys	Trp	Arg	Tyr	His	Gln	Gly	Arg	Asp	Val	Asp	Phe	Glu	195	200	205
Ala	Thr	Trp	Asp	Thr	Val	Arg	Ser	Ile	Val	Leu	Gln	Lys	Phe	Ala	Gly	210	215	220
Pro	Tyr	Asp	Lys	Gly	Glu	Tyr	Ser	Pro	Ser	Val	Gln	Lys	Thr	Leu	Tyr	225	230	235
Asp	Ile	Gln	Val	Leu	Ser	Leu	Ser	Arg	Val	Pro	Glu	Ile	Glu	Asp	Met	245	250	255
Glu	Ile	Ser	Leu	Pro	Asn	Ile	His	Tyr	Phe	Asn	Ile	Asp	Met	Ser	Lys	260	265	270
Met	Gly	Leu	Ile	Asn	Lys	Glu	Glu	Val	Leu	Leu	Pro	Leu	Asp	Asn	Pro	275	280	285
Tyr	Gly	Lys	Ile	Thr	Gly	Thr	Val	Lys	Arg	Lys	Leu	Ser	Ser	Arg	Leu	290	295	300

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<220>  
<221> CDS  
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<220>
<223> Description of Artificial Sequence:pks chimera
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Met	Ala	His	Tyr	Arg	Asn	Asp	Tyr	Lys	Lys	Asn	Asp	Glu	Val	Glu	Phe	
1				5					10					15		
gtc	cga	act	ggc	tat	ggg	aag	gat	atg	ata	aaa	gtt	ctc	cat	att	cag	96
Val	Arg	Thr	Gly	Tyr	Gly	Lys	Asp	Met	Ile	Lys	Val	Leu	His	Ile	Gln	
			20					25					30			

cga gat gga aaa tat cac agc att aaa gag gtg gca act tca gtg caa	144
Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln	
35 40 45	
ctg act ttg agc tcc aaa aaa gat tac ctg cat gga gac aat tca gat	192
Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp	
50 55 60	
gtc atc cct aca gac acc atc aag aac aca gtt aat gtc ctg gcg aag	240
Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys	
65 70 75 80	
ttc aaa ggc atc aaa agc ata gaa act ttt gct gtg act atc tgt gag	288
Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu	
85 90 95	
cat ttc ctt tct tcc ttc aag cat gtc atc aga gct caa gtc tat gtg	336
His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val	
100 105 110	
gaa gaa gtt cct tgg aag cgt ttt gaa aag aat gga gtt aag cat gtc	384
Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val	
115 120 125	
cat gca ttt att tat act cct act gga acg cac ttc tgt gag gtt gaa	432
His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu	
130 135 140	
cag ata agg aat gga cct cca gtc att cat tct gga atc aaa gac cta	480
Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu	
145 150 155 160	
aaa gtc ttg aaa aca acc cag tct ggc ttt gaa gga ttc atc aag gac	528
Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp	
165 170 175	
cag ttc acc acc ctc cct gag gtg aag gac cgg tgc ttt gcc acc caa	576
Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln	
180 185 190	
gtg tac tgc aaa tgg cgc tac cac cag ggc aga gat gtg gac ttt gag	624
Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu	
195 200 205	
gcc acc tgg gac act gtt agg agc att gtc ctg cag aaa ttt gct ggg	672
Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly	
210 215 220	
ccc tat gac aaa ggc gag tac tcg ccc tct gtc cag aag aca ctc tat	720
Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr	
225 230 235 240	
gac atc cag gtg ctc acc ctg ggc cag gtt cct gag ata gaa gat atg	768
Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met	
245 250 255	
gaa atc agc ctg cca aat att cac tac tta aac ata gac atg tcc aaa	816
Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys	
260 265 270	
atg gga ctg atc aac aag gaa gag gtc ttg cta cct tta gac aat cca	864
Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro	
275 280 285	

tat gga aaa att act ggt aca gtc aag agg aag ttg tct tca aga ctg 912  
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 290 295 300

tga 915  
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<210> 4  
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 <212> PRT  
 <213> Artificial Sequence

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 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln  
 35 40 45  
 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp  
 50 55 60  
 Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys  
 65 70 75 80  
 Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu  
 85 90 95  
 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val  
 100 105 110  
 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val  
 115 120 125  
 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu  
 130 135 140  
 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu  
 145 150 155 160  
 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp  
 165 170 175  
 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln  
 180 185 190  
 Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu  
 195 200 205  
 Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly  
 210 215 220  
 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr  
 225 230 235 240  
 Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met  
 245 250 255  
 Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys  
 260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro  
 275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu  
 290 295 300

<210> 5

<211> 304

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: baboon D3H

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Val Arg Thr Gly Tyr Gly Lys Asp Met Val Lys Val Leu His Ile Gln  
 20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln  
 35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp  
 50 55 60

Ile Ile Pro Thr Asp Thr Ile Lys Asn Thr Val His Val Leu Ala Lys  
 65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Ala Phe Gly Val Asn Ile Cys Glu  
 85 90 95

Tyr Phe Leu Ser Ser Phe Asn His Val Ile Arg Ala Gln Val Tyr Val  
 100 105 110

Glu Glu Ile Pro Trp Lys Arg Leu Glu Lys Asn Gly Val Lys His Val  
 115 120 125

His Ala Phe Ile His Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu  
 130 135 140

Gln Leu Arg Ser Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu  
 145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp  
 165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln  
 180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Cys Arg Asp Val Asp Phe Glu  
 195 200 205

Ala Thr Trp Gly Thr Ile Arg Asp Leu Val<sup>g</sup> Leu Glu Lys Phe Ala Gly  
 210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr  
 225 230 235 240

Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met  
 245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys  
 260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro  
 275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu  
 290 295 300

<210> 6  
 <211> 304  
 <212> PRT  
 <213> baboon

<400> 6

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Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln  
 35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp  
 50 55 60

Ile Ile Pro Thr Asp Thr Ile Lys Asn Thr Val His Val Leu Ala Lys  
 65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Ala Phe Gly Val Asn Ile Cys Glu  
 85 90 95

Tyr Phe Leu Ser Ser Phe Asn His Val Ile Arg Ala Gln Val Tyr Val  
 100 105 110

Glu Glu Ile Pro Trp Lys Arg Leu Glu Lys Asn Gly Val Lys His Val  
 115 120 125

His Ala Phe Ile His Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu  
 130 135 140

Gln Leu Arg Ser Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu  
 145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp  
 165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln  
 180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Cys Arg Asp Val Asp Phe Glu  
 195 200 205

Ala Thr Trp Gly Thr Ile Arg Asp Leu Val Leu Glu Lys Phe Ala Gly  
 210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr  
 225 230 235 240

Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met  
 245 250 255



Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys  
260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro  
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Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu  
290 295 300

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<400> 7

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20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln  
35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp  
50 55 60

Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys  
65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu  
85 90 95

His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val  
100 105 110

Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val  
115 120 125

His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu  
130 135 140

Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu  
145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp  
165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln  
180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu  
195 200 205

Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly  
210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr  
225 230 235 240

Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met  
245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys  
260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro  
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Tyr Gly Arg Ile Thr Gly Thr Val Lys Arg Lys Leu Thr Ser Arg Leu  
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20 25 30

Ser Ile Lys Glu Val Ala Thr Ser Val Gln Leu Thr Leu Ser Ser Lys  
35 40 45

Lys Asp Tyr Leu His Gly Asp Asn Ser Asp Val Ile Pro Thr Asp Thr  
50 55 60

Ile Lys Asn Thr Val Asn Val Leu Ala Lys Phe Lys Gly Ile Lys Ser  
65 70 75 80

Ile Glu Thr Phe Ala Val Thr Ile Cys Glu His Phe Leu Ser Ser Phe  
85 90 95

Lys His Val Ile Arg Ala Gln Val Tyr Val Glu Glu Val Pro Trp Lys  
100 105 110

Arg Phe Glu Lys Asn Gly Val Lys His Val His Ala Phe Ile Tyr Thr  
115 120 125

Pro Thr Gly Thr His Phe Cys Glu Val Glu Gln Ile Arg Asn Gly Pro  
130 135 140

Pro Val Ile His Ser Gly Ile Lys Asp Leu Lys Val Leu Lys Thr Thr  
145 150 155 160

Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp Gln Phe Thr Thr Leu Pro  
165 170 175

Glu Val Lys Asp Arg Cys Phe Ala Thr Gln Val Tyr Cys Lys Trp Arg  
180 185 190

Tyr His Gln Gly Arg Asp Val Asp Phe Glu Ala Thr Trp Asp Thr Val  
195 200 205

Arg Ser Ile Val Leu Gln Lys Phe Ala Gly Pro Tyr Asp Lys Gly Glu  
210 215 220

Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr Asp Ile Gln Val Leu Ser  
 225 230 235 240  
 Leu Ser Arg Val Pro Glu Ile Glu Asp Met Glu Ile Ser Leu Pro Asn  
 245 250 255  
 Ile His Tyr Phe Asn Ile Asp Met Ser Lys Met Gly Leu Ile Asn Lys  
 260 265 270  
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 Thr Val Lys Arg Lys Leu Ser Ser Arg Leu  
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 35 40 45  
 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp  
 50 55 60  
 Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys  
 65 70 75 80  
 Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu  
 85 90 95  
 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val  
 100 105 110  
 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val  
 115 120 125  
 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu  
 130 135 140  
 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu  
 145 150 155 160  
 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp  
 165 170 175  
 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln  
 180 185 190  
 Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu  
 195 200 205

Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly  
 210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr  
 225 230 235 240

Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met  
 245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys  
 260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro  
 275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser  
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<211> 298

<212> PRT

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Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe Val Arg Thr Gly Tyr Gly  
 1 5 10 15

Lys Asp Met Ile Lys Val Leu His Ile Gln Arg Asp Gly Lys Tyr His  
 20 25 30

Ser Ile Lys Glu Val Ala Thr Ser Val Gln Leu Thr Leu Ser Ser Lys  
 35 40 45

Lys Asp Tyr Leu His Gly Asp Asn Ser Asp Val Ile Pro Thr Asp Thr  
 50 55 60

Ile Lys Asn Thr Val Asn Val Leu Ala Lys Phe Lys Gly Ile Lys Ser  
 65 70 75 80

Ile Glu Thr Phe Ala Val Thr Ile Cys Glu His Phe Leu Ser Ser Phe  
 85 90 95

Lys His Val Ile Arg Ala Gln Val Tyr Val Glu Glu Val Pro Trp Lys  
 100 105 110

Arg Phe Glu Lys Asn Gly Val Lys His Val His Ala Phe Ile Tyr Thr  
 115 120 125

Pro Thr Gly Thr His Phe Cys Glu Val Glu Gln Ile Arg Asn Gly Pro  
 130 135 140

Pro Val Ile His Ser Gly Ile Lys Asp Leu Lys Val Leu Lys Thr Thr  
 145 150 155 160

Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp Gln Phe Thr Thr Leu Pro  
 165 170 175

Glu Val Lys Asp Arg Cys Phe Ala Thr Gln Val Tyr Cys Lys Trp Arg  
 180 185 190

Tyr His Gln Gly Arg Asp Val Asp Phe Glu Ala Thr Trp Asp Thr Val  
 195 200 205  
 Arg Ser Ile Val Leu Gln Lys Phe Ala Gly Pro Tyr Asp Lys Gly Glu  
 210 215 220  
 Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr Asp Ile Gln Val Leu Thr  
 225 230 235 240  
 Leu Gly Gln Val Pro Glu Ile Glu Asp Met Glu Ile Ser Leu Pro Asn  
 245 250 255  
 Ile His Tyr Leu Asn Ile Asp Met Ser Lys Met Gly Leu Ile Asn Lys  
 260 265 270  
 Glu Glu Val Leu Leu Pro Leu Asp Asn Pro Tyr Gly Lys Ile Thr Gly  
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 Thr Val Lys Arg Lys Leu Ser Ser Arg Leu  
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<210> 11

<211> 301

<212> PRT

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<220>

<223> Description of Artificial Sequence:PKS carboxy truncated

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 20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln  
 35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp  
 50 55 60

Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys  
 65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu  
 85 90 95

His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val  
 100 105 110

Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val  
 115 120 125

His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu  
 130 135 140 145

Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu  
 145 150 155 160

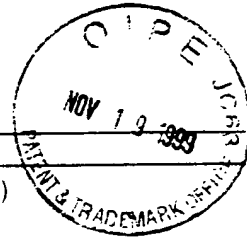
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 165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln  
 180 185 190  
 Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu  
 195 200 205  
 Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly  
 210 215 220  
 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr  
 225 230 235 240  
 Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met  
 245 250 255  
 Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys  
 260 265 270  
 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro  
 275 280 285  
 Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser  
 290 295 300

Serial No.: PCT/US99/17678  
Applicant: Duke University  
Title: PCT/US99/17678

Atty: BJS  
Date: 11-19-99  
Client:  
Ref: 1579-379

\_\_\_\_ Amendment  
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\_\_\_\_ Claims  
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Informal \_\_\_\_\_  
\_\_\_\_ Declaration (\_\_\_\_\_ Pages)  
\_\_\_\_ Assignment  
\_\_\_\_ Priority Document  
\_\_\_\_ Base Issue Fee Transmittal  
\_\_\_\_ Fee (Check)



Other: Sequence Listing pages 37-49  
disk (3.5")